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SEP 17 2001

TECH CENTER 1600/2900

Raw Sequence Listing Error Summary

ERROR DETECTED**SUGGESTED CORRECTION**SERIAL NUMBER: 09/581,651

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence (OLD RULES)
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. (NEW RULES)
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. (NEW RULES)
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or Response
scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 06/04/2001

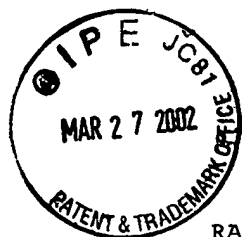
The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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1642

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/581,651

DATE: 08/02/2001
TIME: 17:26:52

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\08022001\I581651.raw

Does Not Comply
Corrected Diskette Needed

See page 6 of 7 A

4 <110> APPLICANT: Schor, Seth Laurence
5 Schor, Ana Maria
7 <120> TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND USES
8 THEREOF
10 <130> FILE REFERENCE: 350013-72
12 <140> CURRENT APPLICATION NUMBER: 09/581,651
13 <141> CURRENT FILING DATE: 2000-10-10
15 <160> NUMBER OF SEQ ID NOS: 15
17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 660
21 <212> TYPE: PRT
22 <213> ORGANISM: Human
24 <400> SEQUENCE: 1
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26 1 5 10 15
27 Leu Asn Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val
28 20 25 30
29 Gln Cys Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys
30 35 40 45
31 Arg Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser
32 50 55 60
33 Gln Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn
34 65 70 75 80
35 Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys
36 85 90 95
37 Tyr Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu
38 100 105 110
39 Glu Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp
40 115 120 125
41 Thr Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile
42 130 135 140
43 Gly Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His
44 145 150 155 160
45 Glu Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His
46 165 170 175
47 Glu Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys
48 180 185 190
49 Gly Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala
50 195 200 205
51 Ala Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln
52 210 215 220
53 Gly Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg
54 225 230 235 240
55 Ile Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr
56 245 250 255
57 Ser Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn

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58          260          265          270
59 Leu Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys
60          275          280          285
61 Glu Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe
62          290          295          300
63 Thr Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro
64          305          310          315          320
65 Pro Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val
66          325          330          335
67 Gly Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr
68          340          345          350
69 Cys Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr
70          355          360          365
71 Tyr Gly Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr
72          370          375          380
73 Asn Asp Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys
74          385          390          395          400
75 Tyr Ser Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly
76          405          410          415
77 Asn Ser Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His
78          420          425          430
79 Asn Tyr Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp
80          435          440          445
81 Cys Gly Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys
82          450          455          460
83 Pro Met Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met
84          465          470          475          480
85 Tyr Arg Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met
86          485          490          495
87 Met Arg Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile
88          500          505          510
89 Ala Tyr Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr
90          515          520          525
91 Asn Val Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu
92          530          535          540
93 Asn Cys Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro
94          545          550          555          560
95 Val Asp Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly
96          565          570          575
97 Asp Ser Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys
98          580          585          590
99 Tyr Gly Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr
100          595          600          605
101 Pro Ser Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser
102          610          615          620
103 Gln Pro Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His
104          625          630          635          640
105 Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg
106          645          650          655

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108 660
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111 <211> LENGTH: 2147
112 <212> TYPE: DNA
113 <213> ORGANISM: Human
115 <400> SEQUENCE: 2
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117 ttaggggtcc ggggcccggt ctgctgctgc tggcctgcca gtgcctgggg acagcgggtgc 120
118 cctccacggg agcctcgaag agcaagaggg aggcctcagca aatgggttcag cccaggtccc 180
119 cgggtggtgt cagtcaaagc aagcccgggt gttatgacaa tggaaaacac tatcagataa 240
120 atcaacagtg ggagcggacc tacctaggca atgcgttggt ttgtacttgt tatggaggaa 300
121 gccgaggttt taactgcgag agtaaacctg aagctgaaga gacttgcttt gacaagtaca 360
122 ctgggaacac ttaccgagtg ggtgacactt atgagcgtcc taaagactcc atgatctggg 420
123 actgtacctg catcgggggt gggcgaggga gaataagctg taccatcgca aaccgctgcc 480
124 atgaaggggg tcagtcctac aagattgggt acacctggag gagaccacat gagactgggtg 540
125 gttacatggt agagtgtgtg tgtcttggtg atggaaaagg agaattggacc tgcaagccca 600
126 tagctgagaa gtgttttgat catgctgctg ggacttccca tgtggtcgga gaaacgtggg 660
127 agaagcccta ccaaggctgg atgatggtag attgtacttg cctgggagaa ggcagcggac 720
128 gcatcacttg cacttctaga aatagatgca acgatcagga cacaaggaca tcctatagaa 780
129 ttggagacac ctggagcaag aaggataatc gaggaaacct gctccagtgc atctgcacag 840
130 gcaacggccg aggagagtgg aagtgtgaga ggcacacctc tgtgcagacc acatcgagcg 900
131 gatctggccc cttaaccgat gtctgtgcag ctgtttacca accgcagcct ccccccagc 960
132 ctctcccta tggccactgt gtcacagaca gtggtgtggt ctactctgtg gggatgcagt 1020
133 ggctgaagac acaaggaaat aagcaaatgc tttgcacgtg cctgggcaac ggagtcagct 1080
134 gccaaagac agctgtaacc cagacttacg gtggcaactc aaatggagag ccatgtgtct 1140
135 taccattcac ctacaacgac aggacggaca gcacaacttc gaattatgag caggaccaga 1200
136 aatactcttt ctgcacagac cacactgttt tggttcagac tcgaggagga aattccaatg 1260
137 gtgccttggt ccacttcccc ttctataaca acaaccacaa ttactatgat tgcacttctg 1320
138 agggcagaag agacaacatg aagtgggtgt ggaccacaca gaactatgat gccgaccaga 1380
139 agtttgggtt ctgccccatg gctgcccacg aggaaatctg cacaaccaat gaaggggtca 1440
140 tgtaccgcat tggagatcag tgggataagc agcatgacat gggtcacatg atgaggtgca 1500
141 cgtgtgttgg gaatggctgt ggggaatgga catgcattgc ctactcgag cttcgagatc 1560
142 agtgcattgt tgatgacatc acttacaatg tgaacgacac attccacaag cgtcatgaag 1620
143 aggggcacat gctgaactgt acatgcttcg gtcagggtcg gggcaggtgg aagtgtgatc 1680
144 ccgtcgacca atgccaggat tcagagactg ggacgtttta tcaaattgga gattcatggg 1740
145 agaagtatgt gcatgggtgc agataccagt gctactgcta tggccgtggc attggggagt 1800
146 ggcattgcca acctttacag acctatccaa gctcaagtgg tctgtcgaa gtatttatca 1860
147 ctgagactcc gagtcagccc aactcccacc ccacccagtg gaatgcacca cagccatctc 1920
148 acatttccaa gtacattctc aggtggagac ctgtgagtat cccaccaga aaccttggat 1980
149 actgagcttc ctaatcttat caattctgat ggtttctttt tttcccagct tttgagccaa 2040
150 caactctgat taactattcc tatagcattt actatatttg tttagtgaac aaacaatatg 2100
151 tggtaatta aattgacttg tagactgaaa aaaaaaaaaa aaaaaaa 2147
153 <210> SEQ ID NO: 3
154 <211> LENGTH: 20
155 <212> TYPE: PRT
156 <213> ORGANISM: Human
158 <400> SEQUENCE: 3
159 Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg

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160      1              5              10              15
161  Asn Leu Gly Tyr
162              20
164 <210> SEQ ID NO: 4
165 <211> LENGTH: 21
166 <212> TYPE: PRT
167 <213> ORGANISM: Human
169 <400> SEQUENCE: 4
170  Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys
171      1              5              10              15
172  Tyr Gly Gly Ser Arg
173              20
175 <210> SEQ ID NO: 5
176 <211> LENGTH: 23
177 <212> TYPE: PRT
178 <213> ORGANISM: Human
180 <400> SEQUENCE: 5
181  Pro Cys Val Leu Pro Phe Thr Tyr Asn Asp Arg Thr Asp Ser Thr Thr
182      1              5              10              15
183  Ser Asn Tyr Glu Gln Asp Gln
184              20
186 <210> SEQ ID NO: 6
187 <211> LENGTH: 20
188 <212> TYPE: PRT
189 <213> ORGANISM: Human
191 <400> SEQUENCE: 6
192  Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser Asn Gly
193      1              5              10              15
194  Ala Leu Cys His
195              20
197 <210> SEQ ID NO: 7
198 <211> LENGTH: 21
199 <212> TYPE: PRT
200 <213> ORGANISM: Human
202 <400> SEQUENCE: 7
203  Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr Ser Gln Leu
204      1              5              10              15
205  Arg Asp Gln Cys Ile
206              20
208 <210> SEQ ID NO: 8
209 <211> LENGTH: 21
210 <212> TYPE: PRT
211 <213> ORGANISM: Human
213 <400> SEQUENCE: 8
214  Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys
215      1              5              10              15
216  Tyr Gly Gly Ser Arg
217              20
219 <210> SEQ ID NO: 9

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PATENT APPLICATION: US/09/581,651

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Input Set : A:\seqlist.txt

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220 <211> LENGTH: 39
221 <212> TYPE: PRT
222 <213> ORGANISM: Human
224 <400> SEQUENCE: 9
225  Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly Arg Thr Phe Tyr Ser
226    1                      5                      10                      15
227  Cys Thr Thr Glu Gly Arg Gln Asp Gly His Leu Trp Cys Ser Thr Thr
228                20                      25                      30
229  Ser Asn Tyr Glu Gln Asp Gln
230                35
232 <210> SEQ ID NO: 10
233 <211> LENGTH: 21
234 <212> TYPE: PRT
235 <213> ORGANISM: Human
237 <400> SEQUENCE: 10
238  Cys Thr Asp His Thr Val Leu Val Gln Thr Gln Gly Gly Asn Ser Asn
239    1                      5                      10                      15
240  Gly Ala Leu Cys His
241                20
243 <210> SEQ ID NO: 11
244 <211> LENGTH: 21
245 <212> TYPE: PRT
246 <213> ORGANISM: Human
248 <400> SEQUENCE: 11
249  Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Tyr Ala Tyr Ser Gln Leu
250    1                      5                      10                      15
251  Arg Asp Gln Cys Ile
252                20
254 <210> SEQ ID NO: 12
255 <211> LENGTH: 20
256 <212> TYPE: PRT
257 <213> ORGANISM: Human
259 <400> SEQUENCE: 12
260  Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg
261    1                      5                      10                      15
262  Trp Lys Glu Ala
263                20
265 <210> SEQ ID NO: 13
266 <211> LENGTH: 11
267 <212> TYPE: PRT
268 <213> ORGANISM: Human
270 <400> SEQUENCE: 13
271  Thr Ala Ser Gly Val Ala Glu Thr Thr Asn Cys
272    1                      5                      10
274 <210> SEQ ID NO: 14
275 <211> LENGTH: 24
276 <212> TYPE: PRT
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:

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US, 9, 581, 651

6 of 7A

<210> 14
<211> 24
<212> PRT
<213> Artificial Sequence

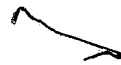
<220>

Description of Artificial
Sequence is mandatory in
Field 223

<400> 14
Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Asp Arg Thr Asp Ser Thr
1 5 10 15
Thr Ser Asn Tyr Glu Gln Asp Gln
20

<210> 15
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> blank



VERIFICATION SUMMARY

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L:281 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: